

5328us.ST25.txt
SEQUENCE LISTING

<110> Sobek, Harald
Frey, Bruno
Antranikian, Garabed
Boehlke, Kristina
Pisani, Francesca Maria
Rossi, Mose

<120> Mutant B-type DNA Polymerases Exhibiting Improved Performance in PCR

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<151> 2000-03-11

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Arg	Ile	Phe	Lys	Lys	Glu	Asn	Gly	Glu	Phe	Lys	Ile	Glu	Leu	Asp	Pro	
			20					25					30			
cat	ttt	cag	ccc	tac	att	tac	gct	ctt	ctc	aaa	gat	gac	tcc	gct	att	144
His	Phe	Gln	Pro	Tyr	Ile	Tyr	Ala	Leu	Leu	Lys	Asp	Asp	Ser	Ala	Ile	
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gat	gaa	ata	aaa	gca	ata	aaa	ggc	gag	aga	cac	gga	aaa	att	gtg	aga	192
Asp	Glu	Ile	Lys	Ala	Ile	Lys	Gly	Glu	Arg	His	Gly	Lys	Ile	Val	Arg	
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Val	Val	Asp	Ala	Val	Lys	Val	Lys	Lys	Lys	Phe	Leu	Gly	Arg	Asp	Val	
65					70					75					80	
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Glu	Val	Trp	Lys	Leu	Ile	Phe	Glu	His	Pro	Gln	Asp	Val	Pro	Ala	Leu	
				85					90					95		
agg	ggc	aag	ata	agg	gaa	cat	cca	gct	gtg	att	gac	att	tat	gag	tac	336
Arg	Gly	Lys	Ile	Arg	Glu	His	Pro	Ala	Val	Ile	Asp	Ile	Tyr	Glu	Tyr	
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gac	ata	ccc	ttt	gcc	aag	cgc	tac	ctc	ata	gac	aag	ggc	ttg	atc	cct	384
Asp	Ile	Pro	Phe	Ala	Lys	Arg	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro	
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Met	Glu	Gly	Asp	Glu	Glu	Leu	Lys	Leu	Met	Ala	Phe	Asp	Ile	Glu	Thr	
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Phe	Tyr	His	Glu	Gly	Asp	Glu	Phe	Gly	Lys	Gly	Glu	Ile	Ile	Met	Ile	
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Asp	Leu	Pro	Tyr	Val	Asp	Val	Val	Ser	Asn	Glu	Arg	Glu	Met	Ile	Lys	
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Tyr	Asn	Gly	Asp	Asn	Phe	Asp	Leu	Pro	Tyr	Leu	Ile	Lys	Arg	Ala	Glu	
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Lys	Leu	Gly	Val	Thr	Leu	Leu	Leu	Gly	Arg	Asp	Lys	Glu	His	Pro	Glu	
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ccc	aag	att	cac	aga	atg	ggc	gat	agc	ttt	gcc	gtg	gaa	att	aaa	ggc	768
Pro	Lys	Ile	His	Arg	Met	Gly	Asp	Ser	Phe	Ala	Val	Glu	Ile	Lys	Gly	
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cca	aca	tac	acg	ctt	gag	gca	gtt	tat	gaa	gcc	gtc	ttg	gga	aaa	acc	864
Pro	Thr	Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Val	Leu	Gly	Lys	Thr	
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aaa	agc	aag	ctg	ggt	gcg	gag	gaa	atc	gcc	gcc	atc	tgg	gaa	aca	gag	912
Lys	Ser	Lys	Leu	Gly	Ala	Glu	Glu	Ile	Ala	Ala	Ile	Trp	Glu	Thr	Glu	
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Asn	Leu	Val	Glu	Trp	Tyr	Leu	Leu	Arg	Val	Ala	Tyr	Glu	Arg	Asn	Glu	
		355					360					365				
ctc	gct	ccg	aac	aag	ccg	gat	gaa	gaa	gag	tac	aga	agg	cgt	tta	agg	1152
Leu	Ala	Pro	Asn	Lys	Pro	Asp	Glu	Glu	Glu	Tyr	Arg	Arg	Arg	Leu	Arg	
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Glu	Asn	Ile	Thr	Tyr	Leu	Asp	Phe	Arg	Cys	Leu	Tyr	Pro	Ser	Ile	Ile	
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gtt	acc	cac	aac	gtc	tcc	cct	gac	act	tta	gaa	aga	gaa	ggc	tgc	aag	1296
Val	Thr	His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Glu	Arg	Glu	Gly	Cys	Lys	
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aat	tac	gat	gtt	gcc	ccg	ata	gta	ggg	tat	aag	ttc	tgc	aag	gat	ttt	1344
Asn	Tyr	Asp	Val	Ala	Pro	Ile	Val	Gly	Tyr	Lys	Phe	Cys	Lys	Asp	Phe	
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ccc	ggt	ttc	att	cca	tct	ata	ctc	ggg	gaa	tta	atc	aca	atg	agg	caa	1392
Pro	Gly	Phe	Ile	Pro	Ser	Ile	Leu	Gly	Glu	Leu	Ile	Thr	Met	Arg	Gln	
	450					455					460					
gaa	ata	aag	aag	aag	atg	aaa	gct	aca	att	gac	cca	ata	gaa	aag	aaa	1440
Glu	Ile	Lys	Lys	Lys	Met	Lys	Ala	Thr	Ile	Asp	Pro	Ile	Glu	Lys	Lys	
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Met	Leu	Asp	Tyr	Arg	Gln	Arg	Ala	Val	Lys	Leu	His	Ala	Asn	Ser	Tyr	
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Tyr	Gly	Tyr	Met	Gly	Tyr	Pro	Lys	Ala	Arg	Trp	Tyr	Ser	Lys	Glu	Cys	
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Ala	Glu	Ser	Val	Thr	Ala	Trp	Gly	Arg	His	Tyr	Ile	Glu	Met	Thr	Ile	
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aaa	gag	ata	gag	gag	aaa	ttt	gga	ttt	aag	gtg	cta	tat	gcc	gac	act	1632
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Asp	Gly	Phe	Tyr	Ala	Thr	Ile	Pro	Gly	Glu	Lys	Pro	Glu	Thr	Ile	Lys	
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Lys	Lys	Ala	Lys	Glu	Phe	Leu	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	
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Arg	Gly	Leu	Glu	Val	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	
	610					615					620					
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Thr	Gln	Ala	Lys	Val	Leu	Glu	Ala	Ile	Leu	Lys	Glu	Asp	Ser	Val	Glu	
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Lys	Ala	Val	Glu	Ile	Val	Lys	Asp	Val	Val	Glu	Glu	Ile	Ala	Lys	Tyr	
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gaa	gtc	ccg	ctt	gaa	aag	ctt	gtt	atc	cac	gag	cag	att	acc	aag	gat	2016
Gln	Val	Pro	Leu	Glu	Lys	Leu	Val	Ile	His	Glu	Gln	Ile	Thr	Lys	Asp	
			660					665					670			
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Leu	Ser	Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Ile	Ala	Lys	Arg	
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Ile	Val	Leu	Arg	Gly	Ser	Gly	Lys	Ile	Ser	Asp	Arg	Val	Ile	Leu	Leu	
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Ser	Glu	Tyr	Asp	Pro	Lys	Lys	His	Lys	Tyr	Asp	Pro	Asp	Tyr	Tyr	Ile	
				725					730				735			
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Glu	Asn	Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Ala	Phe	Gly	
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Tyr	Arg	Lys	Glu	Asp	Leu	Lys	Tyr	Gln	Ser	Ser	Lys	Gln	Val	Gly	Leu	
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35 40 45

Asp Glu Ile Lys Ala Ile Lys Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60

Val Val Asp Ala Val Lys Val Lys Lys Lys Phe Leu Gly Arg Asp Val
65 70 75 80

Glu Val Trp Lys Leu Ile Phe Glu His Pro Gln Asp Val Pro Ala Leu
85 90 95

Arg Gly Lys Ile Arg Glu His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Asp Glu Glu Leu Lys Leu Met Ala Phe Asp Ile Glu Thr
130 135 140

Phe Tyr His Glu Gly Asp Glu Phe Gly Lys Gly Glu Ile Ile Met Ile

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Asp	Leu	Pro	Tyr	Val	Asp	Val	Val	Ser	Asn	Glu	Arg	Glu	Met	Ile	Lys
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Arg	Phe	Val	Gln	Ile	Val	Arg	Glu	Lys	Asp	Pro	Asp	Val	Leu	Ile	Thr
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Leu	Gly	Val	Thr	Leu	Leu	Leu	Gly	Arg	Asp	Lys	Glu	His	Pro	Glu	
225				230					235					240	
Pro	Lys	Ile	His	Arg	Met	Gly	Asp	Ser	Phe	Ala	Val	Glu	Ile	Lys	Gly
				245					250					255	
Arg	Ile	His	Phe	Asp	Leu	Phe	Pro	Val	Val	Arg	Arg	Thr	Ile	Asn	Leu
			260					265					270		
Pro	Thr	Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Val	Leu	Gly	Lys	Thr
		275					280					285			
Lys	Ser	Lys	Leu	Gly	Ala	Glu	Glu	Ile	Ala	Ala	Ile	Trp	Glu	Thr	Glu
	290					295					300				
Glu	Ser	Met	Lys	Lys	Leu	Ala	Gln	Tyr	Ser	Met	Glu	Asp	Ala	Arg	Ala
305					310					315					320
Thr	Tyr	Glu	Leu	Gly	Lys	Glu	Phe	Phe	Pro	Met	Glu	Ala	Glu	Leu	Ala
				325					330					335	
Lys	Leu	Ile	Gly	Gln	Ser	Val	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly

340

345

350

Asn Leu Val Glu Trp Tyr Leu Leu Arg Val Ala Tyr Glu Arg Asn Glu
 355 360 365

Leu Ala Pro Asn Lys Pro Asp Glu Glu Glu Tyr Arg Arg Arg Leu Arg
 370 375 380

Thr Thr Tyr Leu Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp
 385 390 395 400

Glu Asn Ile Thr Tyr Leu Asp Phe Arg Cys Leu Tyr Pro Ser Ile Ile
 405 410 415

Val Thr His Asn Val Ser Pro Asp Thr Leu Glu Arg Glu Gly Cys Lys
 420 425 430

Asn Tyr Asp Val Ala Pro Ile Val Gly Tyr Lys Phe Cys Lys Asp Phe
 435 440 445

Pro Gly Phe Ile Pro Ser Ile Leu Gly Glu Leu Ile Thr Met Arg Gln
 450 455 460

Glu Ile Lys Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Lys Lys
 465 470 475 480

Met Leu Asp Tyr Arg Gln Arg Ala Val Lys Leu His Ala Asn Ser Tyr
 485 490 495

Tyr Gly Tyr Met Gly Tyr Pro Lys Ala Arg Trp Tyr Ser Lys Glu Cys
 500 505 510

Ala Glu Ser Val Thr Ala Trp Gly Arg His Tyr Ile Glu Met Thr Ile
 515 520 525

Lys Glu Ile Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr

530

535

540

Asp Gly Phe Tyr Ala Thr Ile Pro Gly Glu Lys Pro Glu Thr Ile Lys
 545 550 555 560

Lys Lys Ala Lys Glu Phe Leu Lys Tyr Ile Asn Ser Lys Leu Pro Gly
 565 570 575

Leu Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Leu Arg Gly Phe Phe Val
 580 585 590

Ala Lys Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Arg Ile Thr Thr
 595 600 605

Arg Gly Leu Glu Val Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu
 610 615 620

Thr Gln Ala Lys Val Leu Glu Ala Ile Leu Lys Glu Asp Ser Val Glu
 625 630 635 640

Lys Ala Val Glu Ile Val Lys Asp Val Val Glu Glu Ile Ala Lys Tyr
 645 650 655

Gln Val Pro Leu Glu Lys Leu Val Ile His Glu Gln Ile Thr Lys Asp
 660 665 670

Leu Ser Glu Tyr Lys Ala Ile Gly Pro His Val Ala Ile Ala Lys Arg
 675 680 685

Leu Ala Ala Lys Gly Ile Lys Val Arg Pro Gly Thr Ile Ile Ser Tyr
 690 695 700

Ile Val Leu Arg Gly Ser Gly Lys Ile Ser Asp Arg Val Ile Leu Leu
 705 710 715 720

Ser Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Pro Asp Tyr Tyr Ile

